

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:29 ; Search time 20.8151 Seconds
(without alignments)
3900.178 Million cell updates/sec

Title: US-09-836-077-4

Perfect score: 2120
Sequence: 1 MTPPPGRAPASAPRARVLS.....TFQVADSHPEVAQRVERPMGP 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.todent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	907.5	42.8	653	12 Q64906	Q64906 alcelaphine
2	504	23.8	612	12 Q9J5F6	Q9J5F6 fowlpox vir
3	397	18.7	893	4 Q9C0B8	Q9C0B8 homo sapien
4	368.5	17.4	748	4 Q8TB71	Q8TB71 homo sapien
5	359.5	17.0	409	12 Q8OMR4	Q8OMR4 cowpox viru
6	354	16.7	635	4 Q9G6X0	Q9G6X0 homo sapien
7	352.5	16.6	754	4 Q8TDV7	Q8TDV7 homo sapien
8	346	16.3	963	4 Q9C0C4	Q9C0C4 homo sapien
9	345.5	16.3	416	12 Q98VP6	Q98VP6 vaccinia vi
10	342.5	16.2	775	11 Q9OX23	Q9OX23 mus musculu
11	326.5	15.4	457	4 Q9HBR1	Q9HBR1 homo sapien
12	320	15.1	756	13 Q9QGU9	Q9QGU9 gallus gall
13	316.5	14.9	782	4 Q9NS98	Q9NS98 homo sapien
14	308	14.5	1030	4 Q9H2E6	Q9H2E6 homo sapien
15	308	14.5	1049	4 Q9P2H9	Q9P2H9 homo sapien
16	300	14.2	1005	11 Q9EQ71	Q9EQ71 mus musculu

17	298.5	14.1	418	4 Q96J99	Q96J99 homo sapien
18	296	14.0	761	4 Q8WUA9	Q8WUA9 homo sapien
19	281.5	13.3	1202	4 Q9P283	Q9P283 homo sapien
20	279	13.2	284	11 Q54948	Q54948 mus musculu
21	265.5	12.5	1022	4 Q9P249	Q9P249 homo sapien
22	264	12.5	724	5 Q9V707	Q9V707 drosophila
23	263	12.4	296	11 Q9J129	Q9J129 rattus norv
24	256.5	12.1	687	4 Q9BXR8	Q9BXR8 homo sapien
25	253	11.9	770	5 Q44253	Q44253 drosophila
26	253	11.9	770	5 Q9V3M4	Q9V3M4 drosophila
27	252	11.9	616	5 Q9V7P8	Q9V7P8 drosophila
28	251.5	11.9	367	4 Q9HAP9	Q9HAP9 homo sapien
29	248.5	11.7	963	11 Q91Y36	Q91Y36 mus musculu
30	240	11.3	935	4 Q96JF8	Q96JF8 homo sapien
31	229.5	10.8	923	11 Q8R4U3	Q8R4U3 mus musculu
32	225	10.6	920	11 Q8R4U4	Q8R4U4 rattus norv
33	218.5	10.3	228	12 Q9JF56	Q9JF56 vaccinia vi
34	212	10.0	1083	5 Q9V7T0	Q9V7T0 drosophila
35	207	9.8	1081	5 Q9U631	Q9U631 drosophila
36	186	8.8	676	5 Q9RY54	Q9RY54 caenorhabdi
37	169	8.0	658	5 Q95XP4	Q95XP4 caenorhabdi
38	165	7.8	658	5 Q9N138	Q9N138 caenorhabdi
39	160	7.5	264	5 Q95016	Q95016 caenorhabdi
40	137	6.5	1951	5 Q8TA58	Q8TA58 caenorhabdi
41	131	6.2	620	12 Q98329	Q98329 molluscum c
42	127.5	6.0	1944	5 Q9N375	Q9N375 caenorhabdi
43	121	5.7	816	5 Q9V4A7	Q9V4A7 drosophila
44	121	5.7	2051	5 Q96682	Q96682 drosophila
45	115.5	5.4	1963	4 Q75051	Q75051 homo sapien

ALIGNMENTS

1

RESULT 1
Q64906
ID Q64906 PRELIMINARY: PRT: 653 AA.
AC Q64906;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Similar to GENBANK ACCESSION number I26081.
OS Alcelaphine herpesvirus 1 (wildbeest herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=35252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C500;
RX MEDLINE=97201573; PubMed=9049359;
RA Ensser A., Fleckenstein B.;
RT "Alcelaphine herpesvirus type 1 has a semaphorin-like gene."
RN J. Gen. Virol. 76:1063-1067(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C500;
RX MEDLINE=97404659; PubMed=9261371;
RA Ensser A., Pflanz R., Fleckenstein B.;
RT "Primary structure of the alcelaphine herpesvirus 1 genome."
RN J. Virol. 71:6517-6525(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C500;
RA Ensser A., Pflanz R., Fleckenstein B.;
RT Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
RL EMBL: U18243; AAC54475.1; -
DR EMBL: AF005370; AAC58054.1; -
DR InterPro: IPR001627; Sema.
DR Pfam: PF01403; Sema; 1.
SQ SEQUENCE 653 AA: 73645 MW: 5C2816BD567E706E CRC64;
Query Match 42.8%; Score 907.5; DB 12; Length 653;
Best local similarity 48.9%; Pred. No. 8.1e-71;

	Matches	182:	Conservative	54:	Mismatches	129:	Indels	7:	Gaps	5:
QY	22	PARFC-LPRLRLLLFWYAAASAGHSRSGPRISAVMK---	GDHVDFSQREPHTVLFH	77						
Db	45	PAMGTLICVSRILMLI-SAITAAKSRFLDKPRLIVNLTDGFGQ--	HRFGPQGPHTVLFH	102						
QY	78	EGSGFSVMWGGKGVYHNFPEPKNNAVTVTNIGTSGCQDKOCQCGANTITLLRRGNL	137							
Db	103	SLNDSVYVGGNNVTYLFEPFAHSSNASTALINTSTHNTHRLSSTENETITLLHNOTDGL	162							
QY	138	LVCGTNAARPCSMNLVNDVSVMSLGEKMGYAPFSPEDSLVLFEQDEGVSTIRKOEYNGK	197							
Db	163	LACGTNSQKRPSCW-LINNLTITQELGKGLGLAPFSPSSGNLVLEFDQNDITYSTINLYKSLSG	221							
QY	198	IRFRFRICESELVYSIDVWQNPQFIKATIVHODQAYDDKIYFFREDNPDKNPEAPLVN	257							
Db	222	SHKFRIRAGVELVYSIDTGMHRRQFVOATVAVHKNESYDDKIYFFRGQNSHSPQKOPHTV	281							
QY	258	SHVAOLICRDQGGESLSYSKNNFLKALVCSDAATNNENRLODVLFLPPSGOMRT	317							
Db	282	PRVGQVCSDDGGESLSYKWTFLKALACVDYDTGTIVNELDIFLWQAPENSWEET	341							
QY	318	RYVGEFSNPMNYSACVYSYSLGIDIRFRFRSSLKGYHMGLSNRPQCLPKKQPIPTETPQ	377							
Db	342	LTYGLELSPWNSYACVFLTKDIDHVFYSKLNTHHKLPTFRPGCKMNHQVFTETPQ	401							
QY	378	VADSHPEVAQRY	389							
Db	402	VADRYPEVADPV	413							
RESULT 2										
Q9J5F6		PRELIMINARY:	PRT:	612	AA.					
AC	Q9J5F6									
DT	01-OCT-2000 (TREMBlrel. 15, Created)									
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)									
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)									
DE	ORF PFV047 semaphorin vacinia A39R homolog.									
GN	PFV047.									
OS	Fowlpox virus (FPV).									
CC	Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;									
OC	Avipoxvirus.									
OX	NCBI_TaxID=10261;									
RN	(1)									
RN	SEQUENCE FROM N.A.									
RA	MEDLINE=20193820; PubMed=10729156;									
RA	Alfonso C. L., Tulman E. R., Lu Z., Zsak L., Kutish G. F., Rock D. L.;									
RT	"The genome of fowlpox virus."									
RL	J. Virol. 74:3815-3831(2000).									
RN	(2)									
RP	SEQUENCE FROM N.A.									
RA	Alfonso C. L., Tulman E. R., Lu Z., Zsak L., Kutish G. F., Rock D. L.;									
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.									
DR	EMBL: AF198100; AAF44391.1; -									
DR	InterPro: IPR003659; Plexin-like.									
DR	InterPro: IPR002165; Plexin_repeat.									
DR	InterPro: IPR001627; Sema.									
DR	Pfam: PF01437; PSI: 1.									
DR	Pfam: PF01403; Sema: 1.									
DR	SMART: SM00423; PST: 1.									
SO	SEQUENCE 612 AA; 69514 MW; 175D0D1BEC274E23 CRC64;									
Query Match		23.8%;	Score 504;	DB 12;	Length 612;					
Best Local Similarity		37.0%;	Pred. No. 1,66-35;							
Matches 114;	Conservative 57;	Mismatches 107;	Indels 30;	Gaps 9;						
QY	86	VGGRGVYHNFPEPKNAV--RTVNIIGTSGCQDKOCGNVITLLERRNGNLVCGTN	143							
Db	59	IGVNTVTVVVTDTKSNITVDPSPDNVTGSCA-----NYTFIGGYDDKILVCGTN	110							
QY	144	ARKTSCWNLVNDVSVMSLGEKMGYAPFSPEDSLVLFEQDEVYSTIRKQETNGKIPFRFR	203							

Db	111	SSSPCTCW-YINGTIKEPTPYGRGLSPESYDMTGLVLIDGKEIYSTIKK--YSHLSTGEFSR	167
Qy	204	IRESEELYSDIYMONPOFIKATIVHODQAYDDKIYFFREDNPDKNPEAPLNVSRVAOL	263
Db	168	IYKPYLYTSSSTIMKMKPFHLVLSQETNSINTDIYFDEE-----GMATYSRV	217
Qy	264	CRCGDGGESSLVSKMNTPLKAMLVCSDAATNRPRLQDVFLLPPSGQMDRTRYGVF	323
Db	218	CKHDGCGSGSLSSKSTFLKSTINICED-LNVRFYLNKDYVIKQKSP--NETIYGLF	273
Qy	324	SNNWNTSACVYSLGSDIRFRTSSIKGYHMG-LSNRPROMCLPKQPIPTETFOVADSH	382
Db	274	FNEMNTSACVMEFKDIQNNEFTSLKGYSGKVLVSVPQTCI--NTSPRDTEFVYID	331
Qy	383	PEVAQRVE 390	
Db	332	PETLYGVK 339	
RESULT 3			
Q9C0B8	PRELIMINARY:	PRT:	893 AA.
AC	09C0B8:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	KIAI1745 protein (Fragment).		
GN	KIAI1745.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Ox	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21082932; PubMed=11214970;		
RA	Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;		
RT	Prediction of the coding sequences of unidentified human genes. XIX.		
RT	The complete sequences of 100 new cDNA clones from brain which code		
RT	for large proteins in vitro."		
RL	DNA Res. 7:347-355(2000).		
DR	EMBL: AB051532; BAB21836.1; -		
DR	InterPro: IPR003659; Plexin-like.		
DR	InterPro: IPR002165; Plexin-repeat.		
DR	InterPro: IPR001627; Sema.		
DR	Pfam: PF01437; PSI: 1.		
DR	Pfam: PF01403; Sema: 1.		
DR	SMART: SM00423; PSI: 1.		
FT	NON_TER		
SO	SEQUENCE	893 AA; 98361 MW; D6C6CA8DEE524F14 CRC64;	
Query Match			
18.7%; Score 397; DB 4; Length 893;			
Best Local Similarity 30.1%; Pred No. 6.6e-26;			
Matches 129; Conservative 54; Mismatches 167; Indels 78; Gaps 16.			
Qy	3	PPPGRAAPSADRAVL-----SLPARFGLPLRLLLVF-----WVA 41	
Db	42	PEPEPRDTVAALMLKRLTAMGLRSLAAPMGALPRLPRLLLLLLLDQPPPTWALS 101	
Qy	42	ASAGQSHSRGPRISAVMKQGDHVDSPQPP-----HTYLFHEPGSFSSVYVGGKAYHFN 96	
Db	102	-----PRLS-LPLGSEERPLRFEAHISNTALLSRDQRTLYVGAREALFALS 150	
Qy	97	-----FPEGKNASVTRVNIIGSTKSGCDK-----ODCGYI-TLLERRNGLLYGGTNR 145	
Db	151	SNLSTLPGGEIYELLMGADAEKKQCCSRKGPQRCQNTYIKILLPLSSSHLFTGTAIF 210	
Qy	146	KPSCM-NLVNDSVY-----MSLCEMGYAFSPDENSESLVFESGDEVSTIRKQENYK 197	
Db	211	SPMCIYIMMENTLARDEKGNVLLEDGKGRCPFDNFKSTALVVGELY-TGVSSFGQN 269	
Qy	198	IPFRFRIGESLYSDV--MQNQFIKATIVHOD---QAYDDKIYFFREDNPDKNP 251	
Db	270	DPATSRSGSLRTRKSSINMWLQDAFVASAYIPESLGSIGQDDDKIYFFESSETQEEFF 329	

[illegible]

RESULT	ID	PRELIMINARY	PRT	748 AA.
08TB71	08TB71			
AC	08TB71;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Hypothetical 83.0 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=MUSCLE;			
RA	Strausberg R.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC024220; AAH24220.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 748 AA; 83034 MW; 587C35CB65AB4656 CRC64;			

Query Match	17.4%	Score 368.5;	DB 4;	Length 748;
Best Local Similarity	29.0%	Pred. No. 1.6e-23;		
Matches 127; Conservative	49;	Mismatches 167;	Indels 95;	Gaps 18;

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QY 7 GRAPSAAPRAVVLISLPARFGLRLRLRLIVWVAASAQCHSRGSPRISAWMKQDHVDE 66
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 22 GSAPSPRLRL-----SFLQLA-WHOLQFSL 49

QY 67 SÖPEHPTVLFHEPGESVYWGGRKYVHFNPEGKNASVRTVNI-----G 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 50 ERTCSYALLVDEERGRLEFAENHNVASLNL---DNLSKRAKTLAMPAPVEMRECNMAG 108
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 112 STKSCODKOCQGWYITLLER-RONGILYCGTNARKPSC-----WNLVNSYVN----SL 166
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 KDIGT-----ECMNFVKLLHAYNRTHTLLACGTGFHPHPCAEVEYGHAAEEPLKDPGRI 161
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 162 GEMGYAAPESPEDENSLVFEDEYVSTIRKOEYNGKITPFRIRIGESELYT---SDTPWQ 218
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 162 EDGKGKSPYDRHRAASVLTGEEILYSGVADLMGRDPTIFPSLQGRSLRTERHDSKMLN 222
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 219 NPQFICA-TIVHQQDAVDKITYFFREDNPDKNE-APLANSRYAOLCRQDQGESSLV 278
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 EPKFEVAKVFWMIPESENPPDDKIYFFEFRETAEEAALGRLSRYGQICRNVQGORSL-V 286
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 277 SKWNTFLKAMLYVCS-DAATNRNENRRLQDVLLPDPGQMDTIVYGVFSNP--WNNSAV 332
    : : | | | | | | | | | | : : : : : : : : : : : : : : : : : : :
Db 281 NKMTFLFKARLYCVSPGVEGDTHDDQLODQVFL--SSDRHTPLLYAVFSSSTIFQGSAY 338
    : : | | | | | | | | | | : : : : : : : : : : : : : : : : : : :

QY 333 CVYSLGDIDRYF-----RTSLSLKGHMGSLNSPPRGMLPKK-----QPIPET 375
    | | | | | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 CVYSMNQVRAKFLDPRFAKHGEGPMHQWVSYGSRVYPRGMC-PKKTGTGTSSTKDFFDDV 397
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 376 FOYADSHFEVAQRYEPMG 393
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 398 IOFARNHPLMNVSLPTG 415
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 5

ID	Q8QMR4	PRELIMINARY:	PRT:	409 AA.
AC	Q8QMR4;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	169.			
OS	Compx virus (CPV).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
OX	NCBI_TaxID=10243;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RX	MEDLINE=83117629; PubMed=6961398;			
RA	Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;			
RT	"Sequence of terminal region of compox virus DNA: arrangement of			
RT	repeated and unique sequence elements."			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RX	MEDLINE=90177240; PubMed=2309453;			
RA	Parsons B.L., Pickup D.J.;			
RT	"Transcription of orthopoxvirus telomeres at late times during			
RT	infection."			
RL	Virology 175:69-80(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RX	MEDLINE=91196263; PubMed=2014645;			
RA	Hu F.Q., Pickup D.J.;			
RT	"Transcription of the terminal loop region of vaccinia virus DNA is			
RT	initiated from the telomere sequences directing DNA resolution."			
RL	Virology 181:716-720(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RX	MEDLINE=94378510; PubMed=8091665;			
RA	Hu F.Q., Smith C.A., Pickup D.J.;			
RT	"Compx virus contains two copies of an early gene encoding a soluble			
RT	secreted form of the type II TNF receptor."			
RL	Virology 204:343-356(1994).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RA	Pickup D.J.;			
RL	Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRIGHTON RED.			
RA	Dierlich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;			
RL	Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL, AF482758; AAM13617.1.			
SO	SEQUENCE 409 AA; 46488 MW; E14438F5EC68F6F8 CRC64;			
QY	Query Match 17.0%; Score 359.5; DB 12; Length 409;			
	Best Local Similarity 30.4%; Pred. No. 4.2e-23;			
	Matches 95; Conservative 53; Mismatches 129; Indels 35; Gaps 11;			
DB	136 LVTGAGVAYTFPSNELKTKTGLTNNNYITTSIKVEDKD-----TLVCGTN 80			
QY	144 AKRPGCWNLVNDVSVMSLGEKMGYAPSPDENSILVLFEGDEYVSTIRKQYNGKIPRRR 203			
DB	81 NCNPRCWMKIDGSEDEKRNKRGVAPYOKSKYTIITSYNGC-VLSIDINISKEG--IKRMWR 135			
QY	204 IGES--ELITSDTGMONDOFIKATIVYHODQYDDKCIYFFEDNDPDKNPEAPLWVSRYA 261			
DB	136 FGGPGGYDLYTDWYIIPK-DGVRGAFVYDKDGYI-DKYIITLFTDTGSKR---IVKIPYIA 190			
QY	262 QLCRDGCGESSLSVSKWNTFLKAMLVCS-DAAITNRNRLQDVFLDLPDSCQWMDTRVY 320			

QY 262 QICRGDGGESSLSVSKWNTFLKAMLVCS-DAATNRNFNRLODVFLLPDPGQWRDTRVY 320

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Db 191 QMCLEGGPSSLSHRTSTFLKVELECDIGSRQI--IHSKTKTD-----NDTILY 243
QY 321 GFESNPMWNSAVCVSLGIDIRVFRTSLKGYHMGSLNRPQGLPKKOPITETFOVAD 380
Db 244 VFEDSPYSKALCAVSMNSIKOSTTSKLEGTIKQLPSPAFGICLPAGVVPHTTEVIE 303
QY 381 SHPEVAQREVEPM 392
Db 304 KYNVLDDIKPL 315

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RESULT 6

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Q96GX0 PRELIMINARY: PRT: 635 AA.
AC Q96GX0:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Unknown (protein for MGC:18122).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strussberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009113; AAH09113.1;
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR001627; Sema.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF01403; Sema; 1.
SQ SEQUENCE 635 AA: 70694 MW: D994099B476B9210 CRC64;

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Query Match 16.7%; Score 354; DB 4; Length 635;
 Best Local Similarity 34.1%; Pred. No. 2.4e-22;
 Matches 104; Conservative 39; Mismatches 122; Indels 40; Gaps 13;

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QY 125 NYITLLER-RGNGILVCGTNARKPSC-----WNLVNDSVYM-----SLGEMGYAPSPDE 174
Db 2 NFKVLLHAYNRTLLACGAFHPTCAFEVGHRAEPEVLRDLDPGRTEIDGKSKSPYDPNH 61
QY 175 NSLVLFEGDEVSTIRKQENYNGKIPFRIRIGSESELYT---SDTVWQNPQFIKA-TIVVQ 230
Db 62 RAASVLVGEELTSGVAADLMGRDFTIFRSLGQRPRLRTEPHDSRMLNEKFFKAVFWIPPS 121
QY 231 DOAYDDKIYFFREDNPDKNPE-APLNVSRVQLCRGDGGESSLSVSKWNTFLKAMLYC 289
Db 122 ENPDDDKITFFPRETAVEAPALGRLSVRVQICRNDVGGRSL-VNKKWTFPLKARLYC 180
QY 290 S--DAATNFRNRLDDVFLPDPGGMWRDTRVYGVFSNP--WNYSACVYSLGIDIRVF- 344
Db 181 SVPGVEGDHFEQLODVFLL--SSRDHRTPLLYAVFTSSITQGSKAVCYSMADVRRARL 238
QY 345 -----RTSLKGYHMGSLNRPQGLPKK-----QPIPTETFOVADSHPEVAQR 388
Db 239 GFPAKKEGPMHQWVSQGVPRPRPGMC-PSKTFGFSSTKDPDDVIOFARNHPLMYNS 297
QY 389 VEPMG 393
Db 298 VLPFG 302

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RESULT 7

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Q8TVD7 PRELIMINARY: PRT: 754 AA.
AC Q8TVD7:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DR Semaphorin 3B.

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GN SEMA 3B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama N.;
RT "Semaphorin 3B (SEMA3B) cDNA."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083186; BAB88870.1;
SQ SEQUENCE 754 AA: 83691 MW: E61FD08C04E9A68E CRC64;

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Query Match 16.6%; Score 352.5; DB 4; Length 754;
 Best Local Similarity 28.4%; Pred. No. 4.1e-22;
 Matches 126; Conservative 50; Mismatches 167; Indels 101; Gaps 19;

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QY 7 GRAASAPARAVLSELPARFGPLRLRLLLVFVVAASAOGHSRSGFRISAVMKGDHVD 66
Db 22 GSAPSPRLRL-----SFOELQA-WHGLQTFSL 49,
QY 67 SQEPRTVLFHEPGSFSVWVGKGYHNPPEGKASVRYNI-----G 111
Db 50 ERTCCYQALLVDEBERGLFVGAEHNHASLNL---DNISRAKKLAWPAVEMRECCNMAG 106
QY 112 STKSCODKQDCGNITLLER-RGNGILVCGTNARKPSC-----WNLVNDSVYM-----SL 161
Db 107 KDIGT-----ECMNFYKLLHAYNRTLLACGAFHPTCAFEVGHRAEPEVLRDLPGRI 161
QY 162 GEMKGYAPSPDENSLVLEGGDEVSTIRKQENYNGKIPFRIRIGSESELYT---SDTVWQ 218
Db 162 EDGKGSPPYDPNRHRAASVLVGEELTSGVAADLMGRDFTIFRSLGQRPRLRTEPHDSRMLN 221
QY 219 NPQFIKA-TIVVQDOAYDDKIYFFREDNPDKNPE-APLNVSRVQLCRGDGGESSLSV 276
Db 222 ERFKAVFENIPSENDDDKITFFPRETAVEAPALGRLSVRVQICRNDVGGRSL-V 280
QY 277 SKWNTFLKAMLYCS--DAATNFRNRL-----QDVFLPDPGGMWRDTRVYGVFSNP--- 326
Db 281 NMWTFPLKARLYCSVPGVEGDHFEQLODVFLL--SSRDHRTPLLYAVFTSSITQSSSI 338
QY 327 WNYSAVCVYSLGIDIRVF-----RTSLKGYHMGSLNRPQGLPKK-----Q 369
Db 339 FQGSACVYSMDVRRARFGPAKKEGPMHQWVSQGVPRPRPGMC-PSKTFGFSSTK 397
QY 370 PIPTETFOVADSHPEVAQREVEPMG 393
Db 398 DRPDDVIOFARNHPLMYNSVLPFG 421

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RESULT 8

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Q9COC4 PRELIMINARY: PRT: 963 AA.
AC Q9COC4:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE KIA1739 protein (Fragment).
GN KIA1739
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21082932; PubMed-11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RL for large proteins in vitro."
DR EMBL: AB051526; BAB21830.1;
DR InterPro: IPR003599; Ig.

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DR InterPro: IPR003600; Ig-like.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002165; Plexin_repeat.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF01437; PSI; 1.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00410; IG-like; 1.
 DR SMART: SM00423; PSI; 1.
 FT NON_TER 1 1.
 SQ SEQUENCE 963 AA; 106735 MW; 3FA37DBBA3483ECE CRC64;

Query Match 16.3%; Score 346; DB 4; Length 963;
 Best local similarity 25.7%; Pred. No. 2,2e-21;
 Matches 127; Conservative 55; Mismatches 177; Indels 136; Gaps 19;

OY 11 PSAP---RAVLSLPAARGLPLRLRL-----33
 DB 64 PEVPLRLARALISMASSGKRLRYPSFLPAAMICLLPGERLGRPRMCGOGLFQK 123
 OY 34 -----LLVFWVA-----AASAGHSRSGPRISAAMK-----QDA 63
 DB 124 PLPIRGFGHLLVWAGAGRGARLRAVERPQSGCPSAAMLTPELATVARRFSQTGIQDF 183
 OY 64 VDSOPEPTVLPHEPGSFWVWGGKGVYHFNFP-----EGKNASVETVN 109
 DB 184 LTLTLPEPTGLL-----VGAREALFAFSEMALELOGAISWEAPVEKTECICD--- 231
 OY 110 IGTSGKSCODKDCGNVITLLE-RRGNGLLVCTNARKPSCMNLVNDVVSLSGEM--K 165
 DB 232 ----KKG-KNOTECFNFIRFLQPYNASHLVCGTVAFOPKCTYVNMULTFLEHGEFEDGK 286
 OY 166 GYAPFSPDENSILFEGDEYVSTIRKOYNGKIPRRIRIGESELTSDV---MONPOF 222
 DB 287 GRCYPRPAKAGLLVDGELYSA-TLNNFLGTETPIILRNKPHHSKTEYLAFWLNPHF 345
 OY 223 IKATIVHOD---QAYDDKIYFFREDNPDKNPEAPLVNRSVATOLCGDGGESSLSVSK 278
 DB 346 VGSAYVPEVSGFTGDDDKYFFFRERAVESDCYAEVAVARVAVCKGDMGAGARTLO-RK 404
 OY 279 WNTFLKAMLVSDAATNRNENRLQDVFLLPDPSGQWEDTRFVYGSFNPMN--YSACVY 335
 DB 405 WTFLEKARLACSAAPNMQLYFNQLOAMHTLQDTS--WHNTTFEGVQMGDMVLSAICEY 462
 OY 336 SLQDIDRVFETSLKGNH-----GLSNPRGMCV-----PKKQPIPETF 376
 DB 463 QLEIDIGRVFE-GPYKEVHEEAOKMDRYTDPSPRPGSCINMHRHGGYSSLELDPNLL 521
 OY 377 QVADSHPEVAQVERP 391
 DB 522 NPYKKHPLMEQVGP 536

RESULT 9
 ID 098VP6 PRELIMINARY; PRT; 416 AA.
 AC 098VP6;
 DT 01-JUN-2001 (Tremblrel, 17, Created)
 DT 01-JUN-2001 (Tremblrel, 17, last sequence update)
 DT 01-OCT-2001 (Tremblrel, 18, last annotation update)
 DE Semaphorin.
 GN A39R.
 OS Vaccinia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_Taxid=10245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BUFFALOFOX.
 RA Gardner J.D., Tschanke D.C., Reading P.C., Smith G.L.;
 RT "Evidence of a Pro-Inflammatory Role for Vaccinia Virus Semaphorin A39R."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ309297; CAC37361.1;
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF01403; Sema; 1.
 SQ SEQUENCE 416 AA; 47125 MW; AFE77F24678F94B5 CRC64;

Query Match 16.3%; Score 345.5; DB 12; Length 416;
 Best local similarity 31.1%; Pred. No. 7,2e-22;
 Matches 98; Conservative 52; Mismatches 126; Indels 39; Gaps 14;

OY 84 VWVGGKGVYHFNPEEGKNASVFTVNIQSGSCODKDCGNVITL--LERRGNGLVC 140
 DB 36 LYTGVNGAVYTF-----NNKLNKT-----GLTN-----NNYITTSIKVEDADKDTLYC 79
 OY 141 GTNARKPSCMNLVNDVVSLSGEMKGYAPSPDENSLVLEGDEYVSTIRKOYNGKIPR 200
 DB 80 GTNNGNPKCKWIDGSDDPKRG--RGYAPYONSKYVITISHNGC-VLSDINISREG--IKR 134
 OY 201 FRRIRGES--ELYTSPTVMONPOFIKATIVHODVADDKIYFFREDNPDKNPEAPLVNS 258
 DB 135 WRPFDEGCGYDLFTADVIRK-DGLRGAIFYDKDGT-DKYIILFTDIGSKR--YKIP 189
 OY 259 RVAQLCRGDDGESSLSVSKWNTFLKAMLVCS-DAATNRNENRLQDVFLLPDPSGQWRT 317
 DB 190 YIAQMCLENDGSPSSLSHRSSTFLKVELCDIDGRSROI--IHSRTIKTD-----NDT 242
 OY 318 RYVGVSFNPMNNAVCYYSIGDIDRVFRTSLGYNHGLSNPRPKGLPKQPIPETRQ 377
 DB 243 ILVVFDPSPYSKSLALCYVSNMTIKQSFSTKLEGYTKQLPSAPAGICLPAGKVPPTTFE 302
 OY 378 VADSHPEVAQVERPM 392
 DB 303 VIEKYNVLDDILKPL 317

RESULT 10
 ID 090X23 PRELIMINARY; PRT; 775 AA.
 AC 090X23;
 DT 01-MAY-2000 (Tremblrel, 13, Created)
 DT 01-MAY-2000 (Tremblrel, 13, last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, last annotation update)
 DE Semaphorin M-Semak.
 GN SEMA3E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57/BLACK 6.
 RA Miyazaki N., Furiyama T., Inagaki S.;
 RT "A novel semaphorin, M-Semak which inhibits neural outgrowth from sensory neurons."
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DE EMBL: AF034744; AAD01996.1;
 DR MGI:1340034; Sema3e.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00423; PSI; 1.
 SQ SEQUENCE 775 AA; 89543 MW; 221E766F404098D4 CRC64;

Query Match 16.2%; Score 342.5; DB 11; Length 775;
 Best local similarity 28.3%; Pred. No. 3,2e-21;
 Matches 126; Conservative 65; Mismatches 160; Indels 95; Gaps 23;
 OY 13 APRARVLSLPARGLPLRLLLVFWVAASAGHSRSGPRISAVWKGQDHDV---FSQ 68
 DB 2 APAGHILITL-----LLMGHLLLELWTPRGHSA---NPSYRLRLSKHELLELRTSIFOS 51

